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Actinomycin-D

drug conc. (mM) 1 0.25 .062 .016 .004 .001 .00025 nil control

Distamycin A

drug conc. (mM) 1 0.25 .062 .016 .004 .001 .00025 nil control

Ethidium Bromide

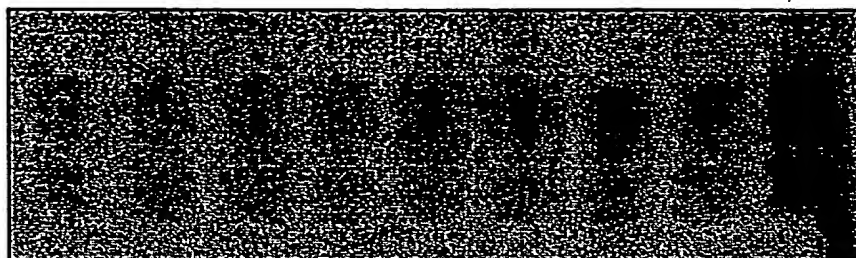
drug conc. (mM) 1 0.25 .062 .016 .004 .001 .00025 nil control

SSB

protein conc. (μ g/well) 50 12.5 3.12 .78 .20 .05 .012 nil control

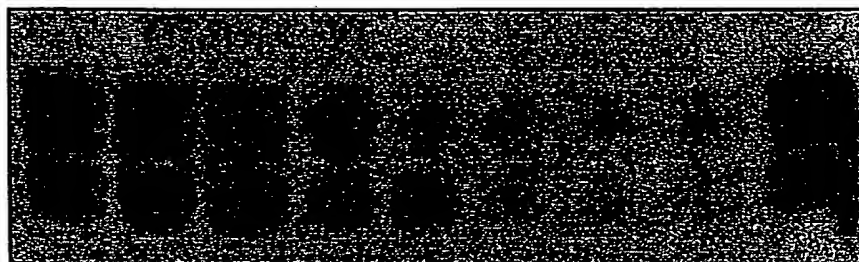
Figure 1. Titration of 4 DNA binders in a DNA hybridization reaction. Dark bands indicate unbound target (higher band intensity = less bound target). The control shows the total intensity of unbound target.

Distamycin A



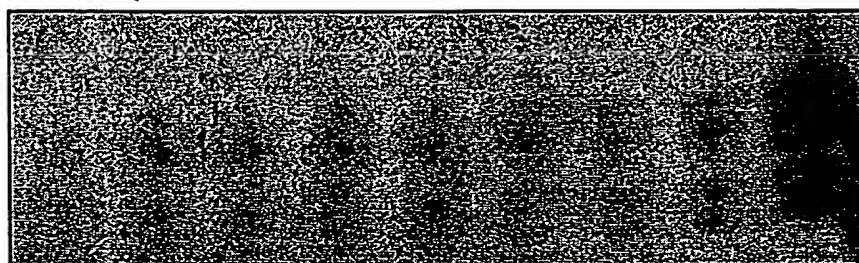
drug conc. (mM) 1 0.25 .062 .016 .004 .001 .00025 nil control

**Distamycin A+
Actinomycin D**



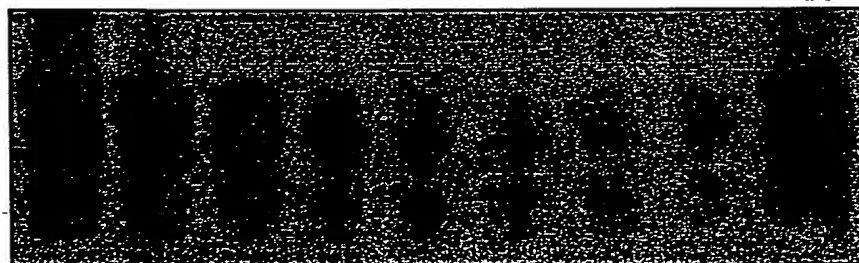
drug conc. (mM) 1 0.25 .062 .016 .004 .001 .00025 nil control

**Distamycin A+
Ethidium
Bromide**



drug conc. (mM) 1 0.25 .062 .016 .004 .001 .00025 nil control

**Distamycin A+
SSB**



protein conc, (µg/well) 50 12.5 3.12 .78 .20 .05 .012 nil control

Figure 2. Titration of 4 DNA binder combinations in a DNA hybridization reaction. Distamycin A was held constant at 1 mM for those sets with drug combinations.

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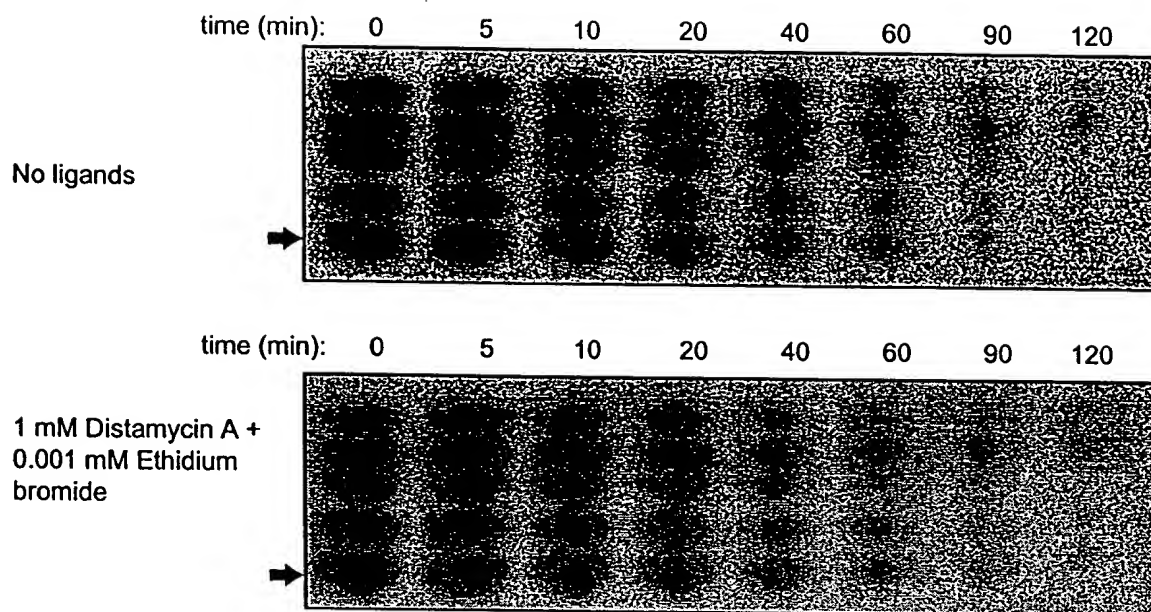


Figure 3a. Time dependence of hybridization in the presence and absence of distamycin A and ethidium bromide. The arrow indicates the perfect matched probe. The hairpin and target sequences are listed in the inset. Dark bands indicate unbound target; higher band intensity, less bound target.

Figure 1 consists of five vertically stacked line graphs, each representing a different HBV strain: hbv-23, hbv-21, hbv-19, hbv-17, and hbv-15. The y-axis for all graphs is 'fraction bound' ranging from 0.0 to 1.0. The x-axis is 'time (min)' ranging from 0 to 120. Each graph contains two data series: one represented by open circles and another by filled circles. Both series show an increase in the fraction bound over time, with the filled circles generally showing a faster rate of binding.

Time (min)	hbv-23 (open)	hbv-23 (filled)	hbv-21 (open)	hbv-21 (filled)	hbv-19 (open)	hbv-19 (filled)	hbv-17 (open)	hbv-17 (filled)	hbv-15 (open)	hbv-15 (filled)
0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
5	0.05	0.02	0.02	0.01	0.10	0.05	0.10	0.05	0.10	0.05
10	0.08	0.12	0.05	0.08	0.12	0.15	0.12	0.15	0.15	0.18
20	0.20	0.20	0.15	0.18	0.22	0.25	0.25	0.20	0.25	0.25
40	0.30	0.55	0.28	0.42	0.42	0.62	0.42	0.52	0.45	0.55
60	0.52	0.65	0.42	0.52	0.60	0.72	0.60	0.68	0.62	0.70
90	0.78	0.75	0.68	0.65	0.88	0.92	0.88	0.92	0.92	0.95
120	0.92	0.95	0.85	0.85	1.00	1.00	1.00	1.00	1.00	1.00

Figure 3b. Plot of normalized binding curves from figure 3. Gray circles indicate hybridization without DNA ligands; black circles indicate hybridization in 1 mM distamycin A and 0.001 mM ethidium bromide.

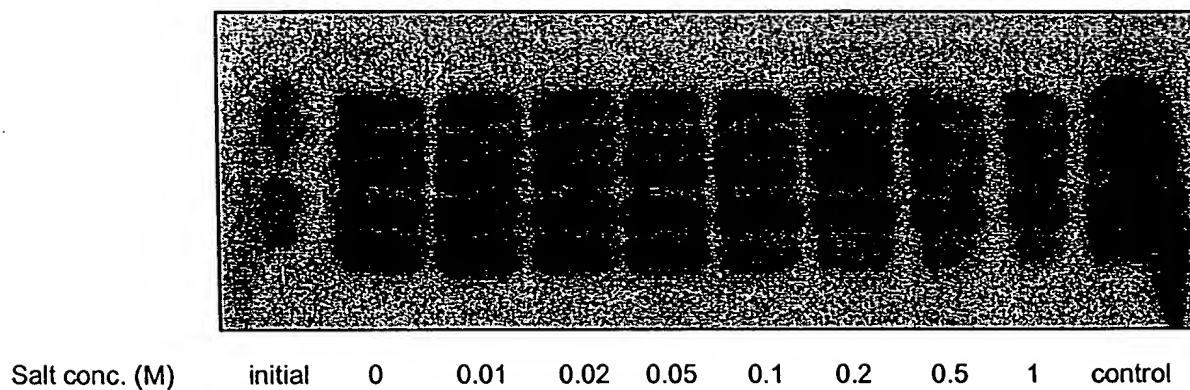
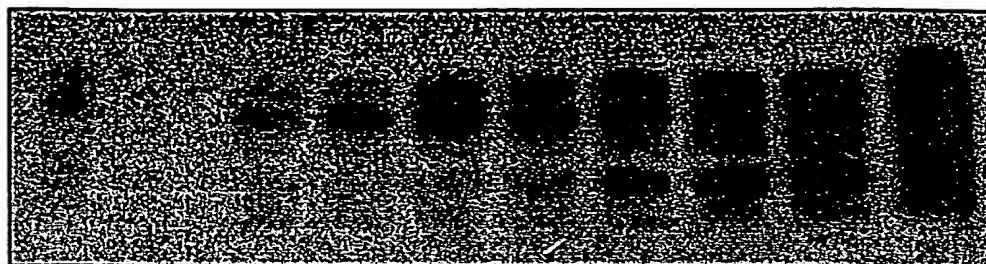


Figure 4. Salt concentration dependence of denaturation at 40% (v/v) formamide. The buffer was 10 mM phosphate, pH 7.2 + specified concentration of NaCl. Wash Incubation time was held constant (1 h).

**No
Distamycin A**



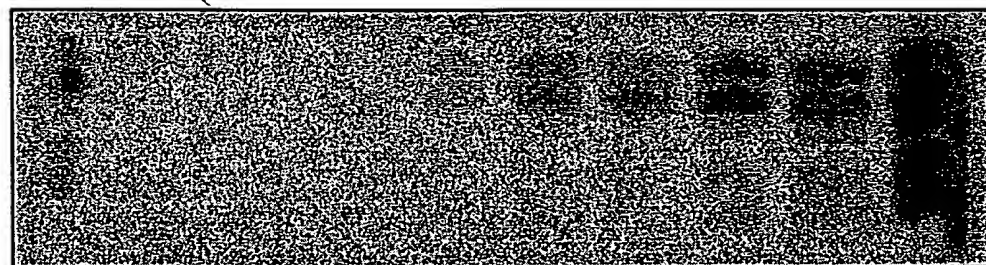
% Formamide initial 0 20 22.5 25 27.5 30 32.5 35 control

**0.062 mM
Distamycin A**



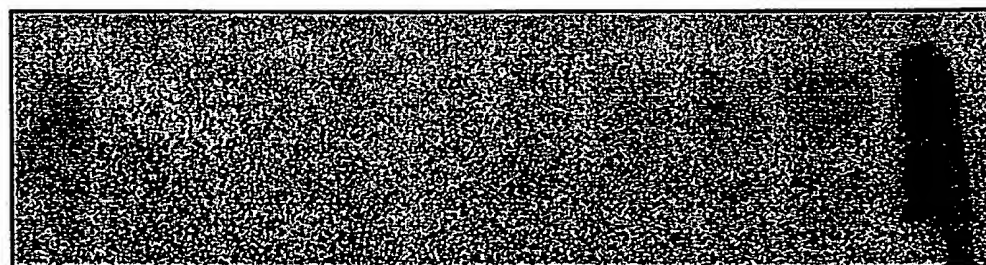
% Formamide initial 0 20 22.5 25 27.5 30 32.5 35 control

**0.25 mM
Distamycin A**



% Formamide initial 0 20 22.5 25 27.5 30 32.5 35 control

**1 mM
Distamycin A**

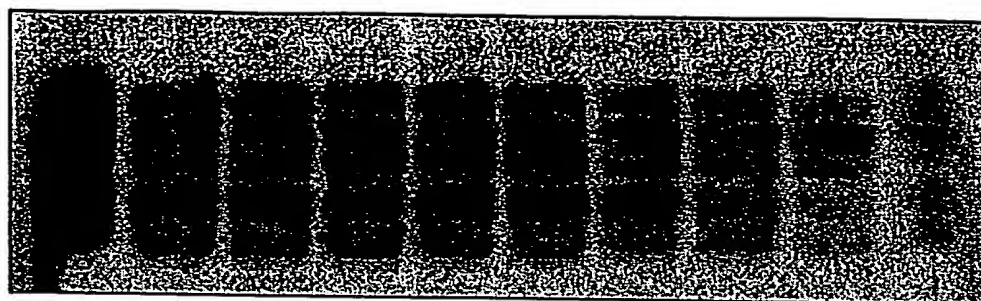


% Formamide initial 0 20 22.5 25 27.5 30 32.5 35 control

Figure 5a. Formamide concentration is cross-titered with Distamycin A in the wash buffer. Darker bands indicate a higher degree of dissociation.

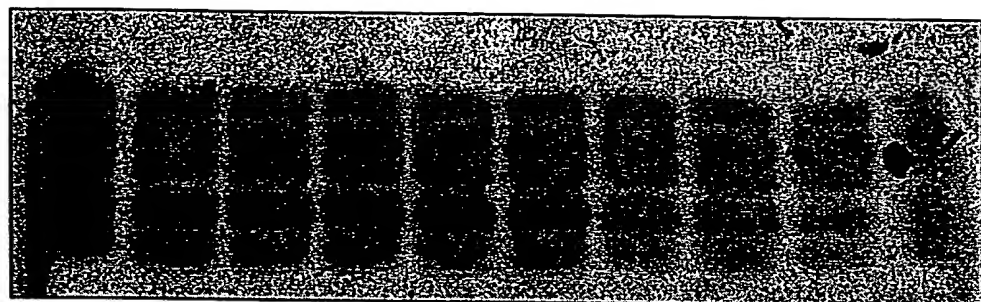
003747164.13200

**No
Distamycin A**



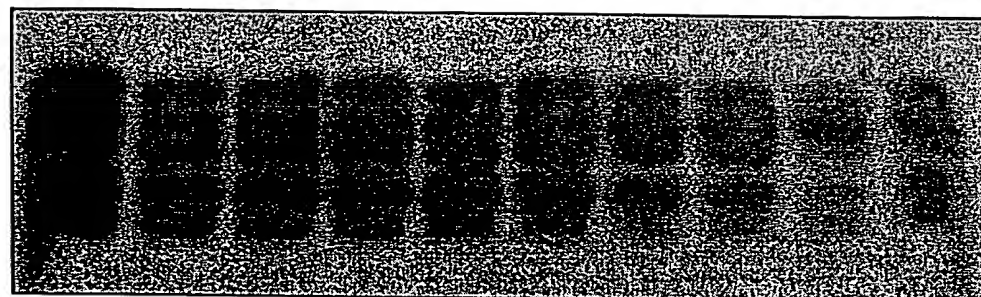
time (min) control 60 40 30 20 15 10 5 0 initial

**0.062 mM
Distamycin A**



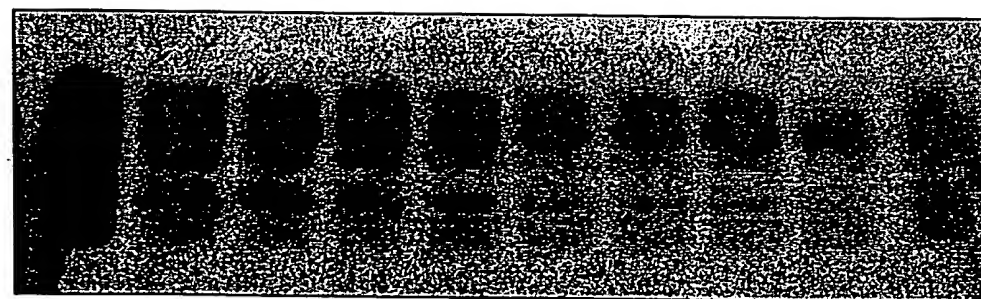
time (min) control 60 40 30 20 15 10 5 0 initial

**0.25 mM
Distamycin A**



time (min) control 60 40 30 20 15 10 5 0 initial

**1 mM
Distamycin A**



time (min) control 60 40 30 20 15 10 5 0 initial

Figure 6. Time dependence of denaturation at 40% (v/v) formamide, as a function of Distamycin A concentration. Darker bands indicate higher degree of denaturation.

